

## SEQUENCE LISTING

<110> MASURE, STEFAN  
RICHARDSON, ALAN

<120> HUMAN AKT-3

<130> JAB-1458

<140> 09/869,079

<141> 1999-12-17

<150> PCT/GB99/04311

<151> 1999-12-17

<160> 16

<170> PatentIn Ver. 3.2

<210> 1

<211> 1547

<212> DNA

<213> Homo sapiens

<400> 1

```

gggagtcac atgagcgcgt ttaccattgt gaaagaaggt tgggttcaga agaggggaga 60
atatataaaa aactggaggc caagatactt ccttttgaag acagatggct cattcatagg 120
atataaagag aaacctcaag atgtggattt accttatccc ctcaacaact ttccagtggc 180
aaaatgccag ttaatgaaaa cagaacgacc aaagccaaac acatttataa tcagatgtct 240
ccagtggact actgttatag agagaacatt tcatgtagat actccagagg aaaggggaaga 300
atggacagaa gctatccagg ctgtagcaga cagactgcag aggcaagaag aggagagaat 360
gaattgtagt ccaacttcac aaattgataa tataggagag gaagagatgg atgcctctac 420
aaccatcat aaaagaaaaga caatgaatga ttttgactat ttgaaactac taggtaaagg 480
cacttttggg aaagttatth tggttcgaga gaaggcaagt ggaaaatact atgctatgaa 540
gattctgaag aaagaagtca ttattgcaaa ggatgaagtg gcacacactc taactgaaaag 600
cagagtatta aagaacacta gacatccctt tttaacatcc ttgaaatatt ccttcagac 660
aaaagaccgt ttgtgttttg tgatggaata tgttaaatggg ggcgagctgt tttccattt 720
gtcgagagag cgggtgttct ctgaggaccg cacacgtttc tatgggtgcag aaattgtctc 780
tgcttggac tatctacatt ccggaaagat tgtgtaccgt gatctcaagt tggagaatct 840
aatgctggac aaagatggcc acataaaaat tacagatttt ggactttgca aagaagggat 900
cacagatgca gccaccatga agacattctg tggcactcca gaatatctgg caccagaggt 960
gttagaagat aatgactatg gccgagcagt agactggtgg ggcctagggg ttgtcatgta 1020
tgaaatgatg tgtgggaggt tacctttcta caaccaggac catgagaaac tttttgaatt 1080
aatattaatg gaagacatta aatttcctcg aacactctct tcagatgcaa aatcattgct 1140
ttcagggtc ttgataaagg atccaaataa acgccttggg ggaggaccag atgatgcaaa 1200
agaaattatg agacacagtt tcttctctgg agtaaaactgg caagatgtat atgataaaaa 1260
gcttgatcct ccttttaaac ctcaagtaac atctgagaca gatactagat attttgatga 1320
agaatttaca gctcagacta ttacaataac accacctgaa aaatatgatg aggatggtat 1380
ggactgcagt gacaatgaga ggcggccgca tttccctcaa ttttctact ctgcaagtgg 1440
acgagaataa gtctctttca ttctgctact tcactgtcat cttcaattta ttactgaaaa 1500
tgattcctgg acatcaccag tcctagctct tacacatagc aggggca 1547

```

<210> 2

<211> 1436

<212> DNA

<213> Homo sapiens

&lt;400&gt; 2

```

atgagcgatg ttaccattgt gaaagaaggt tgggttcaga agagggggaga atatataaaa 60
aactggaggc caagatactt ccttttgaag acagatggct cattcatagg atataaagag 120
aaacctcaag atgtggattt accttatccc ctcaacaact ttccagtggc aaaatgccag 180
ttaatgaaaa cagaacgacc aaagccaaac acatttataa tcagatgtct ccagtggact 240
actgttatag agagaacatt tcatgtagat actccagagg aaaggaaga atggacagaa 300
gctatccagg ctgtagcaga cagactgcag aggcaagaag aggagagaat gaattgtagt 360
ccaacttcac aaattgataa tataggagag gaagagatgg atgcctctac aacccatcat 420
aaaagaaaaga caatgaatga ttttgactat ttgaaactac taggtaaagg cacttttggg 480
aaagttattt tggttcgaga gaaggcaagt ggaaaatact atgctatgaa gattctgaag 540
aaagaagtca ttattgcaaa ggatgaagtg gcacacactc taactgaaag cagagtatta 600
aagaacacta gacatccctt tttaacatcc ttgaaatatt ccttccagac aaaagaccgt 660
ttgtgttttg tgatggaata tgtaaatggg ggcgagctgt ttttccattt gtcgagagag 720
cgggtgttct ctgaggaccg cacacgtttc tatggtgcag aaattgtctc tgccttggac 780
tatctacatt ccggaaagat tgtgtaccgt gatctcaagt tggagaatct aatgctggac 840
aaagatggcc acataaaaaat tacagatttt ggacttttgc aagaagggat cacagatgca 900
gccaccatga agacattctg tggcactcca gaatatctgg caccagaggt gttagaagat 960
aatgactatg gccgagcagt agactggtgg ggcctagggg ttgtcatgta tgaaatgatg 1020
tgtgggaggt taccttttcta caaccaggac catgagaaac tttttgaatt aatattaatg 1080
gaagacatta aatttcctcg aacactctct tcagatgcaa aatcattgct ttcagggctc 1140
ttgataaagg atccaaataa acgccttggg ggaggaccag atgatgcaaa agaaattatg 1200
agacacagtt tcttctctgg agtaaaactgg caagatgtat atgataaaaa gcttgtacct 1260
ccttttaaac ctcaagtaac atctgagaca gatactagat attttgatga agaatttaca 1320
gctcagacta ttacaataac accacctgaa aaatatgatg aggatgggat ggactgcatg 1380
gacaatgaga ggcggccgca tttccctcaa ttttctact ctgcaagtga acgaga 1436

```

&lt;210&gt; 3

&lt;211&gt; 479

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

```

Met Ser Asp Val Thr Ile Val Lys Glu Gly Trp Val Gln Lys Arg Gly
 1              5              10              15

Glu Tyr Ile Lys Asn Trp Arg Pro Arg Tyr Phe Leu Leu Lys Thr Asp
      20              25              30

Gly Ser Phe Ile Gly Tyr Lys Glu Lys Pro Gln Asp Val Asp Leu Pro
      35              40              45

Tyr Pro Leu Asn Asn Phe Ser Val Ala Lys Cys Gln Leu Met Lys Thr
      50              55              60

Glu Arg Pro Lys Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp Thr
      65              70              75              80

Thr Val Ile Glu Arg Thr Phe His Val Asp Thr Pro Glu Glu Arg Glu
      85              90              95

Glu Trp Thr Glu Ala Ile Gln Ala Val Ala Asp Arg Leu Gln Arg Gln
      100             105             110

Glu Glu Glu Arg Met Asn Cys Ser Pro Thr Ser Gln Ile Asp Asn Ile
      115             120             125

```

Gly	Glu	Glu	Glu	Met	Asp	Ala	Ser	Thr	Thr	His	His	Lys	Arg	Lys	Thr	130	135	140
Met	Asn	Asp	Phe	Asp	Tyr	Leu	Lys	Leu	Leu	Gly	Lys	Gly	Thr	Phe	Gly	145	150	155
Lys	Val	Ile	Leu	Val	Arg	Glu	Lys	Ala	Ser	Gly	Lys	Tyr	Tyr	Ala	Met	165	170	175
Lys	Ile	Leu	Lys	Lys	Glu	Val	Ile	Ile	Ala	Lys	Asp	Glu	Val	Ala	His	180	185	190
Thr	Leu	Thr	Glu	Ser	Arg	Val	Leu	Lys	Asn	Thr	Arg	His	Pro	Phe	Leu	195	200	205
Thr	Ser	Leu	Lys	Tyr	Ser	Phe	Gln	Thr	Lys	Asp	Arg	Leu	Cys	Phe	Val	210	215	220
Met	Glu	Tyr	Val	Asn	Gly	Gly	Glu	Leu	Phe	Phe	His	Leu	Ser	Arg	Glu	225	230	235
Arg	Val	Phe	Ser	Glu	Asp	Arg	Thr	Arg	Phe	Tyr	Gly	Ala	Glu	Ile	Val	245	250	255
Ser	Ala	Leu	Asp	Tyr	Leu	His	Ser	Gly	Lys	Ile	Val	Tyr	Arg	Asp	Leu	260	265	270
Lys	Leu	Glu	Asn	Leu	Met	Leu	Asp	Lys	Asp	Gly	His	Ile	Lys	Ile	Thr	275	280	285
Asp	Phe	Gly	Leu	Cys	Lys	Glu	Gly	Ile	Thr	Asp	Ala	Ala	Thr	Met	Lys	290	295	300
Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	Val	Leu	Glu	Asp	305	310	315
Asn	Asp	Tyr	Gly	Arg	Ala	Val	Asp	Trp	Trp	Gly	Leu	Gly	Val	Val	Met	325	330	335
Tyr	Glu	Met	Met	Cys	Gly	Arg	Leu	Pro	Phe	Tyr	Asn	Gln	Asp	His	Glu	340	345	350
Lys	Leu	Phe	Glu	Leu	Ile	Leu	Met	Glu	Asp	Ile	Lys	Phe	Pro	Arg	Thr	355	360	365
Leu	Ser	Ser	Asp	Ala	Lys	Ser	Leu	Leu	Ser	Gly	Leu	Leu	Ile	Lys	Asp	370	375	380
Pro	Asn	Lys	Arg	Leu	Gly	Gly	Gly	Pro	Asp	Asp	Ala	Lys	Glu	Ile	Met	385	390	395
Arg	His	Ser	Phe	Phe	Ser	Gly	Val	Asn	Trp	Gln	Asp	Val	Tyr	Asp	Lys	405	410	415
Lys	Leu	Val	Pro	Pro	Phe	Lys	Pro	Gln	Val	Thr	Ser	Glu	Thr	Asp	Thr	420	425	430

Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro  
 435 440 445

Pro Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp Asn Glu Arg  
 450 455 460

Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Arg Glu  
 465 470 475

<210> 4

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 primer

<400> 4

accatttctc caagttgggg gctcag

26

<210> 5

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 primer

<400> 5

gggagtcac atgagcgatg ttacc

25

<210> 6

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 primer

<400> 6

cactccagaa tatctggcac cagagg

26

<210> 7

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 primer

<400> 7  
ctatggccga gcagtagact ggtgg 25

<210> 8  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 8  
tgcccctgct atgtgtaaga gctagg 26

<210> 9  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 9  
aagagctagg actggtgatg tccagg 26

<210> 10  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 10  
tgaaggtcgg agtcaacgga tttggt 26

<210> 11  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 11  
gggttgtaga ggcattcatc tcttcc 26

<210> 12  
 <211> 28  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
 Tyr Asp Glu Asp Gly Met Asp Cys Met Asp Asn Glu Arg Arg Pro His  
     1                    5                    10                    15  
 Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Arg Glu  
                     20                    25

<210> 13  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic (HA)  
           tag

<400> 13  
 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala  
     1                    5

<210> 14  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           primer

<400> 14  
 catgtgggcc atgaggtcca ccac

24

<210> 15  
 <211> 480  
 <212> PRT  
 <213> Homo sapiens

<400> 15  
 Met Ser Asp Val Ala Ile Val Lys Glu Gly Trp Leu His Lys Arg Gly  
     1                    5                    10                    15  
 Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Asn Asp  
                     20                    25                    30  
 Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro Gln Asp Val Asp Gln Arg  
                     35                    40                    45  
 Glu Ala Pro Leu Asn Asn Phe Ser Val Ala Gln Cys Gln Leu Met Lys  
     50                    55                    60

Thr	Glu	Arg	Pro	Arg	Pro	Asn	Thr	Phe	Ile	Ile	Arg	Cys	Leu	Gln	Trp	65	70	75	80
Thr	Thr	Val	Ile	Glu	Arg	Thr	Phe	His	Val	Glu	Thr	Pro	Glu	Glu	Arg	85	90	95	
Glu	Glu	Trp	Thr	Thr	Ala	Ile	Gln	Thr	Val	Ala	Asp	Gly	Leu	Lys	Lys	100	105	110	
Gln	Glu	Glu	Glu	Glu	Met	Asp	Phe	Arg	Ser	Gly	Ser	Pro	Ser	Asp	Asn	115	120	125	
Ser	Gly	Ala	Glu	Glu	Met	Glu	Val	Ser	Leu	Ala	Lys	Pro	Lys	His	Arg	130	135	140	
Val	Thr	Met	Asn	Glu	Phe	Glu	Tyr	Leu	Lys	Leu	Leu	Gly	Lys	Gly	Thr	145	150	155	160
Phe	Gly	Lys	Val	Ile	Leu	Val	Lys	Glu	Lys	Ala	Thr	Gly	Arg	Tyr	Tyr	165	170	175	
Ala	Met	Lys	Ile	Leu	Lys	Lys	Glu	Val	Ile	Val	Ala	Lys	Asp	Glu	Val	180	185	190	
Ala	His	Thr	Leu	Thr	Glu	Asn	Arg	Val	Leu	Gln	Asn	Ser	Arg	His	Pro	195	200	205	
Phe	Leu	Thr	Ala	Leu	Lys	Tyr	Ser	Phe	Gln	Thr	His	Asp	Arg	Leu	Cys	210	215	220	
Phe	Val	Met	Glu	Tyr	Ala	Asn	Gly	Gly	Glu	Leu	Phe	Phe	His	Leu	Ser	225	230	235	240
Arg	Glu	Arg	Val	Phe	Ser	Glu	Asp	Arg	Ala	Arg	Phe	Tyr	Gly	Ala	Glu	245	250	255	
Ile	Val	Ser	Ala	Leu	Asp	Tyr	Leu	His	Ser	Glu	Lys	Asn	Val	Val	Tyr	260	265	270	
Arg	Asp	Leu	Lys	Leu	Glu	Asn	Leu	Met	Leu	Asp	Lys	Asp	Gly	His	Ile	275	280	285	
Lys	Ile	Thr	Asp	Phe	Gly	Leu	Cys	Lys	Glu	Gly	Ile	Lys	Asp	Gly	Ala	290	295	300	
Thr	Met	Lys	Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	Val	305	310	315	320
Leu	Glu	Asp	Asn	Asp	Tyr	Gly	Arg	Ala	Val	Asp	Trp	Trp	Gly	Leu	Gly	325	330	335	
Val	Val	Met	Tyr	Glu	Met	Met	Cys	Gly	Arg	Leu	Pro	Phe	Tyr	Asn	Gln	340	345	350	
Asp	His	Glu	Lys	Leu	Phe	Glu	Leu	Ile	Leu	Met	Glu	Glu	Ile	Arg	Phe	355	360	365	

Pro Arg Thr Leu Gly Pro Glu Ala Lys Ser Leu Leu Ser Gly Leu Leu  
 370 375 380  
 Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly Gly Ser Glu Asp Ala Lys  
 385 390 395 400  
 Glu Ile Met Gln His Arg Phe Phe Ala Gly Ile Val Trp Gln His Val  
 405 410 415  
 Tyr Glu Lys Lys Leu Ser Pro Pro Phe Lys Pro Gln Val Thr Ser Glu  
 420 425 430  
 Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile Thr  
 435 440 445  
 Ile Thr Pro Pro Asp Gln Asp Asp Ser Met Glu Cys Val Asp Ser Glu  
 450 455 460  
 Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Thr Ala  
 465 470 475 480

<210> 16  
 <211> 481  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
 Met Asn Glu Val Ser Val Ile Lys Glu Gly Trp Leu His Lys Arg Gly  
 1 5 10 15  
 Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Ser Asp  
 20 25 30  
 Gly Ser Phe Ile Gly Tyr Lys Glu Arg Pro Glu Ala Pro Asp Gln Thr  
 35 40 45  
 Leu Pro Pro Leu Asn Asn Phe Ser Val Ala Glu Cys Gln Leu Met Lys  
 50 55 60  
 Thr Glu Arg Pro Arg Pro Asn Thr Phe Val Ile Arg Cys Leu Gln Trp  
 65 70 75 80  
 Thr Thr Val Ile Glu Arg Thr Phe His Val Asp Ser Pro Asp Glu Arg  
 85 90 95  
 Glu Glu Trp Met Arg Ala Ile Gln Met Val Ala Asn Ser Leu Lys Gln  
 100 105 110  
 Arg Ala Pro Gly Glu Asp Pro Met Asp Tyr Lys Cys Gly Ser Pro Ser  
 115 120 125  
 Asp Ser Ser Thr Thr Glu Glu Met Glu Val Ala Val Ser Lys Ala Arg  
 130 135 140



Ala	Lys	Val	Thr	Met	Asn	Asp	Phe	Asp	Tyr	Leu	Lys	Leu	Leu	Gly	Lys	
145					150					155					160	
Gly	Thr	Phe	Gly	Lys	Val	Ile	Leu	Val	Arg	Glu	Lys	Ala	Thr	Gly	Arg	
				165					170					175		
Tyr	Tyr	Ala	Met	Lys	Ile	Leu	Arg	Lys	Glu	Val	Ile	Ile	Ala	Lys	Asp	
			180					185					190			
Glu	Val	Ala	His	Thr	Val	Thr	Glu	Ser	Arg	Val	Leu	Gln	Asn	Thr	Arg	
		195					200					205				
His	Pro	Phe	Leu	Thr	Ala	Leu	Lys	Tyr	Ala	Phe	Gln	Thr	His	Asp	Arg	
	210					215					220					
Leu	Cys	Phe	Val	Met	Glu	Tyr	Ala	Asn	Gly	Gly	Glu	Leu	Phe	Phe	His	
225					230					235					240	
Leu	Ser	Arg	Glu	Arg	Val	Phe	Thr	Glu	Glu	Arg	Ala	Arg	Phe	Tyr	Gly	
				245					250					255		
Ala	Glu	Ile	Val	Ser	Ala	Leu	Glu	Tyr	Leu	His	Ser	Arg	Asp	Val	Val	
			260					265						270		
Tyr	Arg	Asp	Ile	Lys	Leu	Glu	Asn	Leu	Met	Leu	Asp	Lys	Asp	Gly	His	
		275					280					285				
Ile	Lys	Ile	Thr	Asp	Phe	Gly	Leu	Cys	Lys	Glu	Gly	Ile	Ser	Asp	Gly	
	290					295					300					
Ala	Thr	Met	Lys	Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	
305					310					315					320	
Val	Leu	Glu	Asp	Asn	Asp	Tyr	Gly	Arg	Ala	Val	Asp	Trp	Trp	Gly	Leu	
				325					330					335		
Gly	Val	Val	Met	Tyr	Glu	Met	Met	Cys	Gly	Arg	Leu	Pro	Phe	Tyr	Asn	
			340					345					350			
Gln	Asp	His	Glu	Arg	Leu	Phe	Glu	Leu	Ile	Leu	Met	Glu	Glu	Ile	Arg	
		355					360					365				
Phe	Pro	Arg	Thr	Leu	Ser	Pro	Glu	Ala	Lys	Ser	Leu	Leu	Ala	Gly	Leu	
	370					375					380					
Leu	Lys	Lys	Asp	Pro	Lys	Gln	Arg	Leu	Gly	Gly	Gly	Pro	Ser	Asp	Ala	
385					390					395					400	
Lys	Glu	Val	Met	Glu	His	Arg	Phe	Phe	Leu	Ser	Ile	Asn	Trp	Gln	Asp	
				405					410					415		
Val	Val	Gln	Lys	Lys	Leu	Leu	Pro	Pro	Phe	Lys	Pro	Gln	Val	Thr	Ser	
				420				425					430			
Glu	Val	Asp	Thr	Arg	Tyr	Phe	Asp	Asp	Glu	Phe	Thr	Ala	Gln	Ser	Ile	
		435					440					445				

Thr Ile Thr Pro Pro Asp Arg Tyr Asp Ser Leu Gly Leu Leu Glu Leu  
450 455 460

Asp Gln Arg Thr His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Ile Arg  
465 470 475 480

Glu